SEQUENCE LISTING

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<110> RIPAMONTI, UGO
      RAMOSHEBI, LENTSHA N.
<120> METHODS FOR INDUCING ANGIOGENESIS USING MORPHOGENIC
      PROTEINS AND STIMULATORY FACTORS
<130> STK-6
<140>
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<160> 10
<170> PatentIn Vent.
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<210> 1
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<212> DNA
<213> Homo sapiens
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<221> CDS
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                                                        Met His Val
cgc tca ctg cga gct gcg gcg dcg cac agc ttc gtg gcg ctc tgg gca
                                                                       105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
                          10
ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
gag gtg cac tcg age ttc atc cac cgg cgc ctc cgc age cag gag cgg
                                                                       201
Glu Val His Ser Ser Phe Ile His Arg Leu Arg Ser Gln Glu Arg
egg gag atg cag ege gag ate ete tee att ttg gge ttg eee eae ege
                                                                       249
Arg Glu Met Gln Arg Glu Ile Leu Ser Tle Leu Gly Leu Pro His Arg
ccg cgc ccg cac ctc cag ggc aag cac aad tcg gca ccc atg ttc atg
                                                                       297
Pro Arg Pro His Leu Gln Gly Lys His Asn\Ser Ala Pro Met Phe Met
                               75
ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc
Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly
                          90
gge cag ggc ttc tcc tac ccc tac aag gcc gtc\ttc agt acc cag ggc
Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val \Phe Ser Thr Gln Gly
                     105
                                          110
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		`		120					125					130		
	gtc Val															489
	cca Pro															537
	gaa Glu 165															585
	atc Ile															633
	gtg Val															681
gac Asp	agc Ser	cgt Arg	acc Thr 215	ctc Leu	tgg Trp	gdc	tcg Ser	gag Glu 220	gag Glu	ggc Gly	tgg Trp	ctg Leu	gtg Val 225	ttt Phe	gac Asp	729
	aca Thr															777
ggc Gly	ctg Leu 245	cag Gln	ctc Leu	tcg Ser	gtg Val	gag Glu 250	acg Thr	ctg Leu	gat Asp	glà aaa	cag Gln 255	agc Ser	atc Ile	aac Asn	ccc Pro	825
	ttg Leu															873
ttc Phe	atg Met	gtg Val	gct Ala	ttc Phe 280	ttc Phe	aag Lys	gcc Ala	acg Thr	gag Glu 285	gtc Val	cac His	ttc Phe	cgc Arg	agc Ser 290	atc Ile	921
cgg Arg	tcc Ser	acg Thr	999 Gly 295	agc Ser	aaa Lys	cag Gln	cgc Arg	agc Ser 300	cag Gln	aac Asn	cgc Arg	tcc Ser	aag Lys 305	acg Thr	ccc Pro	969
aag Lys	aac Asn	cag Gln 310	gaa Glu	gcc Ala	ctg Leu	cgg Arg	atg Met 315	gcc Ala	aac Asn	gtg Val	gca Ala	gag Glu 320	aāc Asn	agc Ser	agc Ser	1017
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cga gac ttg ggc ttg cag gac ttg Arg Asp Leu Gly Trp Gln Asp Trp 340 345		Pro Glu Gly		1113
gcc tac tac tgt gag ggg gag tgt Ala Tyr Tyr Cys Glu Gly Glu Cys 360	_	_	_	1161
aac gcc acc aac cac gcc atc gtg Asn Ala Thr Asn His Ala Ile Val			e Ile Asn	1209
ccg gaa acg gtg ccc aag ccc tgc Pro Glu Thr Val Pro Lys Pro Cys 390 395	Cys Ala Pro		_	1257
atc tcc gtc ctc tac ttc gat gac Ile Ser Val Leu Tyr Phe Asp Asp 405 410				1305
tac aga aac atg gtg gtc cgg gcc Tyr Arg Asn Met Val Val Arg Ala 420		His	ctcc	1351
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<210> 2

<211> 431

<212> PRT

<213> Homo sapiens

<400> 2

Met His Val Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala
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Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro 70 Met Phe Met Leù Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr 120 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys 135 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu 155 Ser Lys Ile Pro Glu Gly 🗘 u Ala Val Thr Ala Ala Glu Phe Arg Ile 170 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile 185 Ser Val Tyr Gln Val Leu Gln ∂_t lu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu 215 220 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg 230 235 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser 250 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn 265 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe 280 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser 295 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp tle Ile Ala Pro Glu 345 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn

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Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
   370
                       375
Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
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Leu Asn Ala Ild Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
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<223> each Xaa is independently selected from a group of
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     the specification
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                                   10
Asp Trp Xaa Ile Ala Pro Xaa \wply Tyr Xaa Ala Tyr Tyr Cys Glu Gly
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Pro Xaa Xaa Val Pro Lys
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
                    70
Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
Xaa Ala Cys Gly Cys His
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<213> Artificial Sequence
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<223> each Xaa is independently selected from a group of
     one or more specified amino acids as defined in
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Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa
Pro Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                 70
Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
Xaa
<210> 5
<211> 102
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Generic-Seq-8
<220>
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     specification
<400> 5
Cys Xaa Xaa Xaa Leu Xaa Xaa\ Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
                               10
Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
                        40
```

Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Xaa Xaa Met Xaa Val

75

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Xaa Xaa Cys Xaa Cys Xaa
       100
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<211> 97
<212> PR1
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<223> Description of Artificial Sequence: Generic-Seq-9
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<223> each Kaa is independently selected from a group of
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   the specification
. 10
Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa
35
                  40
55
70
                         75
Xaa
<210> 7
<211> 102
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Generic-Seq-10
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   specification
<400> 7
10
                                   15
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```
Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly
          20
40
Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa
Xaa Xaa Cys Xaa Cys Xaa
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<211> 5
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<400> 8
Cys Xaa Xaa Xaa Xaa
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<211> 5
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<400> 9
Cys Xaa Xaa Xaa Xaa
<210> 10
<211> 102
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Generic Sequence

<220>

<223> each Xaa represents any amino acid residue

<400> 10

Cys Xaa Xaa Xaa Xaa Leu Xaa Val Xaa Phe Xaa Asp Xaa Glu Trp Xaa 1 10 15

Xaa Trp Xaa Xaa Xaa Pro Xaa Gly Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
20 25 30

Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala

Xaa Xaa Gln Xaa Xaa Val Xaa Xaa Xaa Asn Xaa Xaa Xaa Asa Pro Xaa 50 60

Xaa Cys Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa 65 70 80

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa Xaa Tyr Xaa Xaa Met Xaa Val

Xaa Xaa Cys Xaa Cys Xaa 100